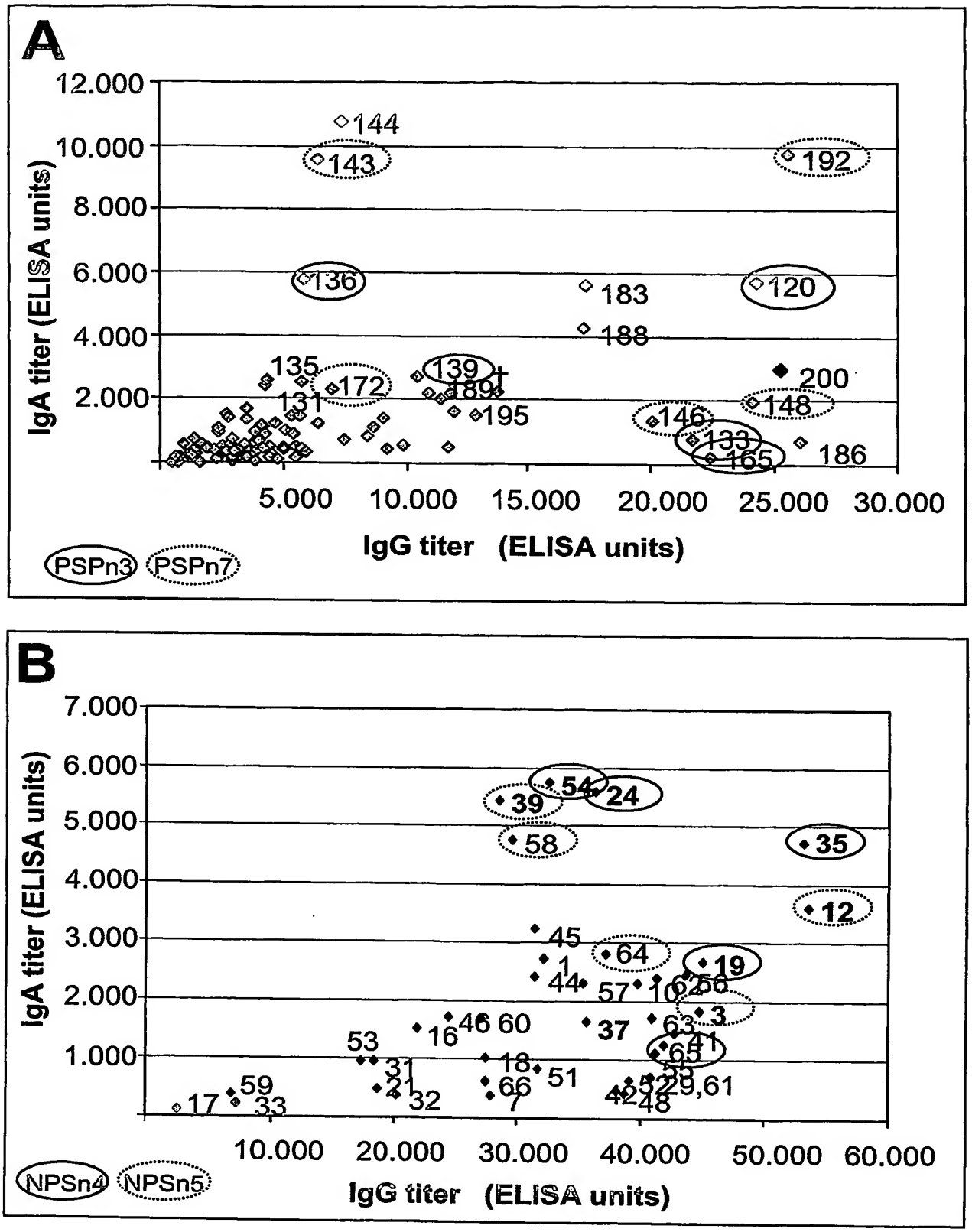
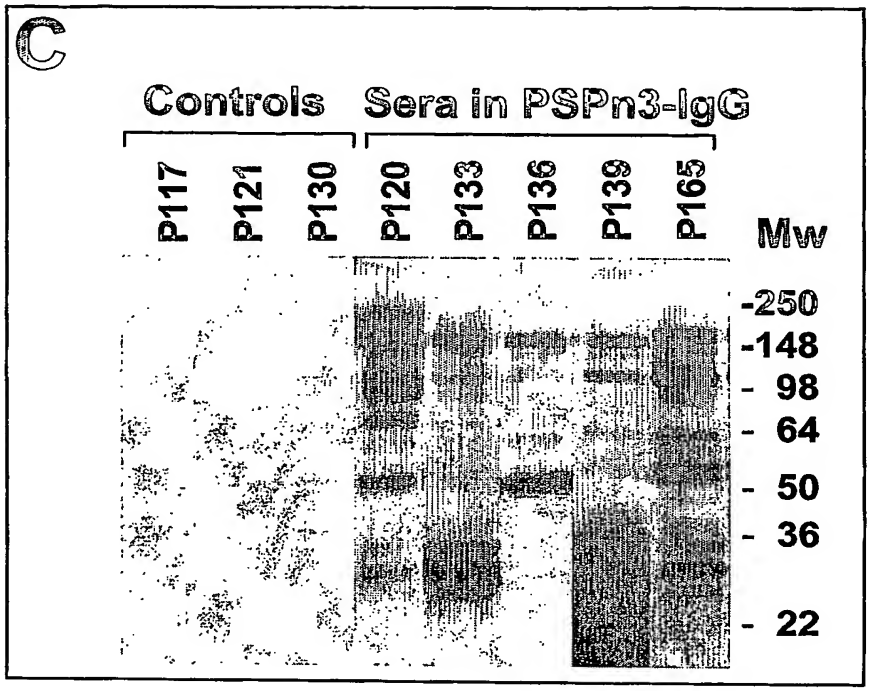


Fig. 1


C
Controls
Sera in PSPn3-IgG
P117
P121
P130
P120
P133
P136
P139
P165
Mw
-250
-148
- 98
- 64
- 50
- 36
- 22

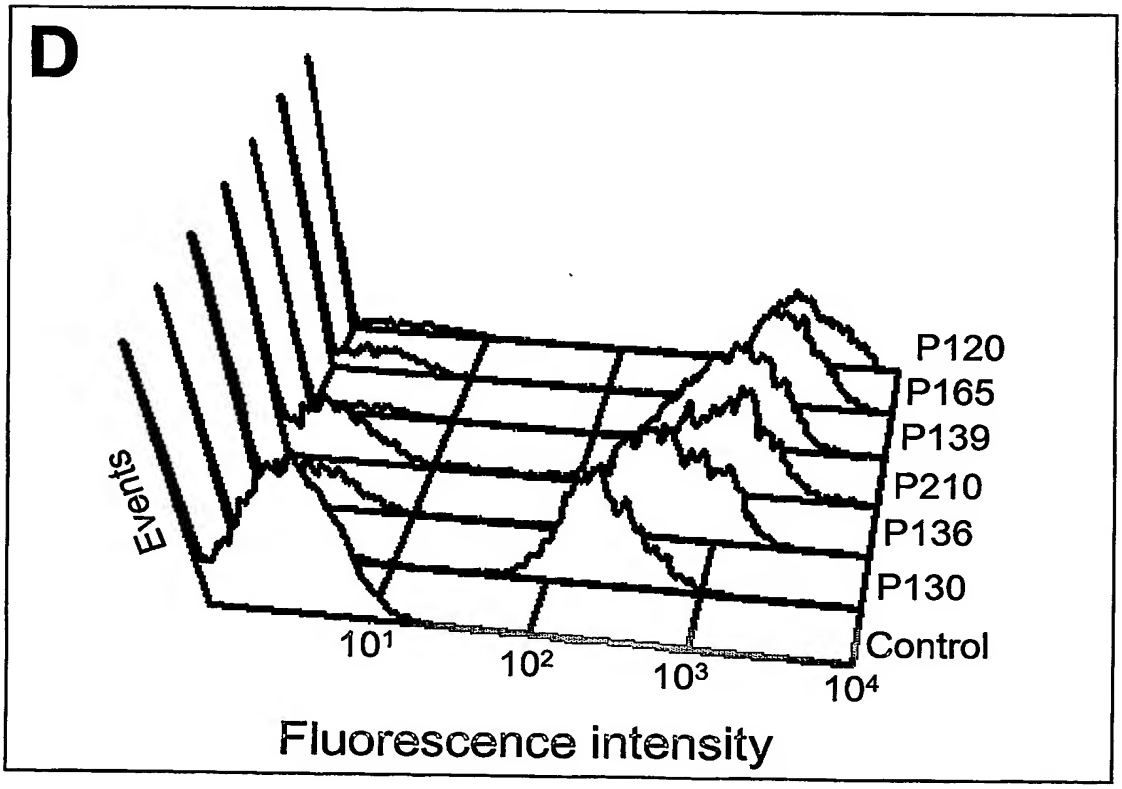

D
Events
P120
P165
P139
P210
P136
P130
Control
10¹
10²
10³
10⁴
Fluorescence intensity

Fig.1

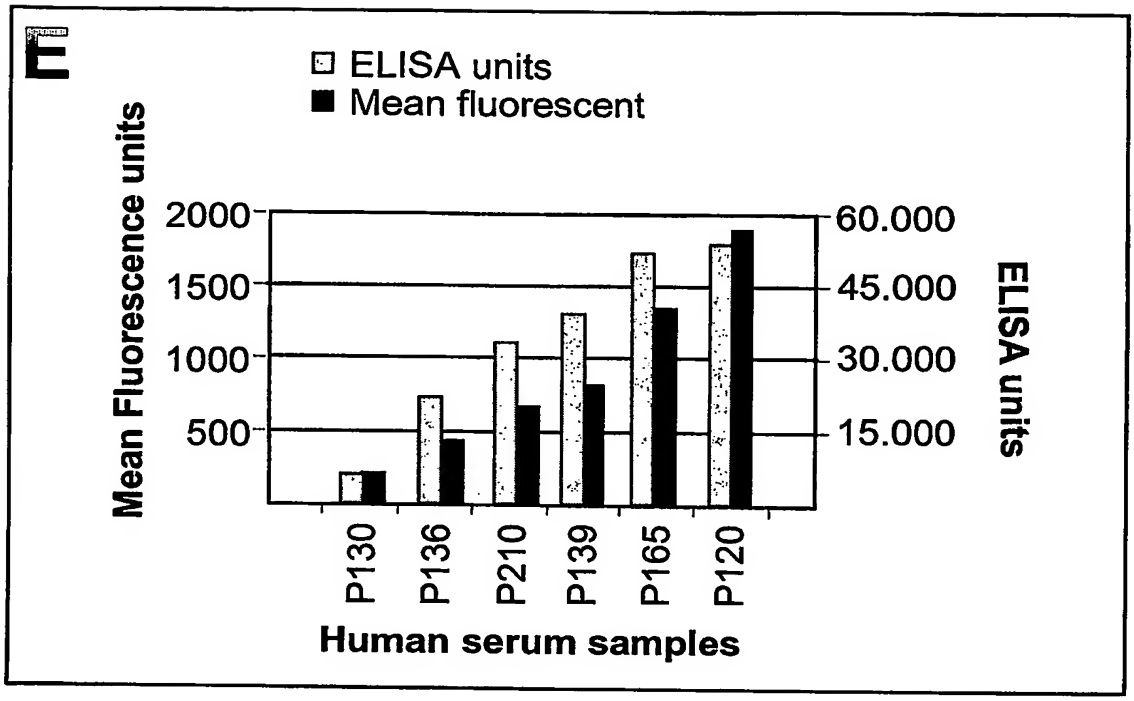
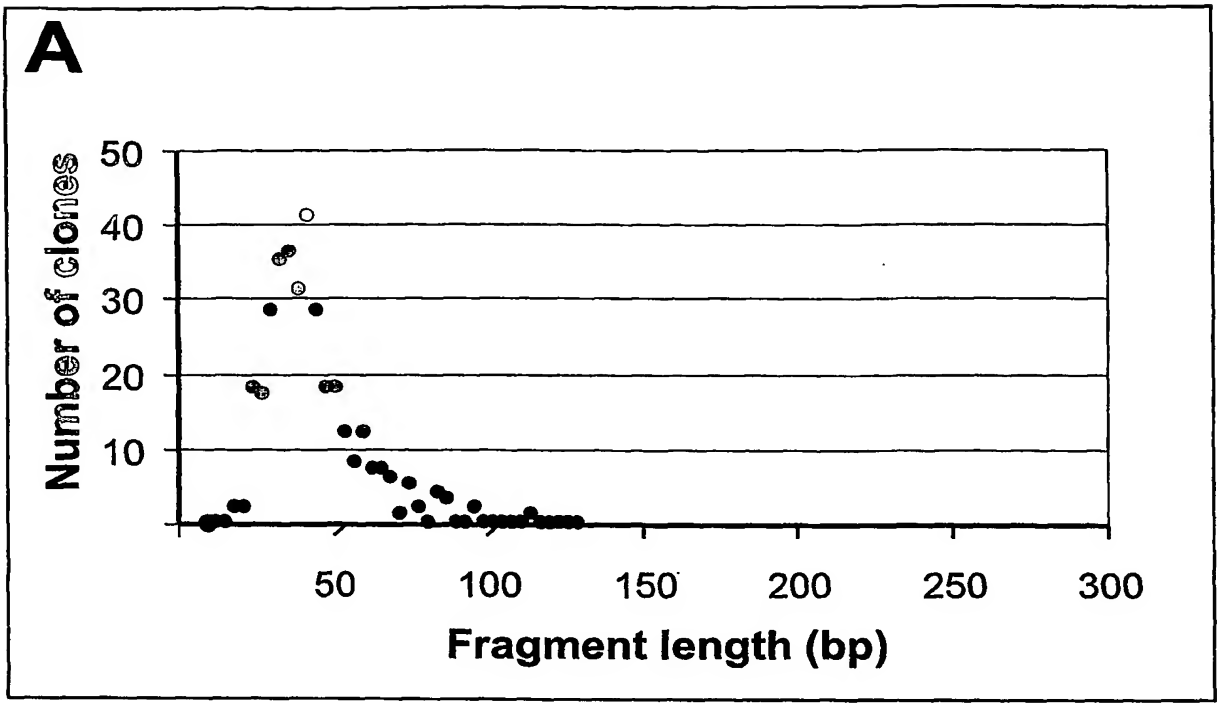

ELISA units
Mean fluorescent
Mean Fluorescence units
2000
1500
1000
500
60.000
45.000
30.000
15.000
ELISA units
P130
P136
P210
P139
P165
P120
Human serum samples

Fig.1


A
Number of clones
50
40
30
20
10
50
100
150
200
250
300
Fragment length (bp)

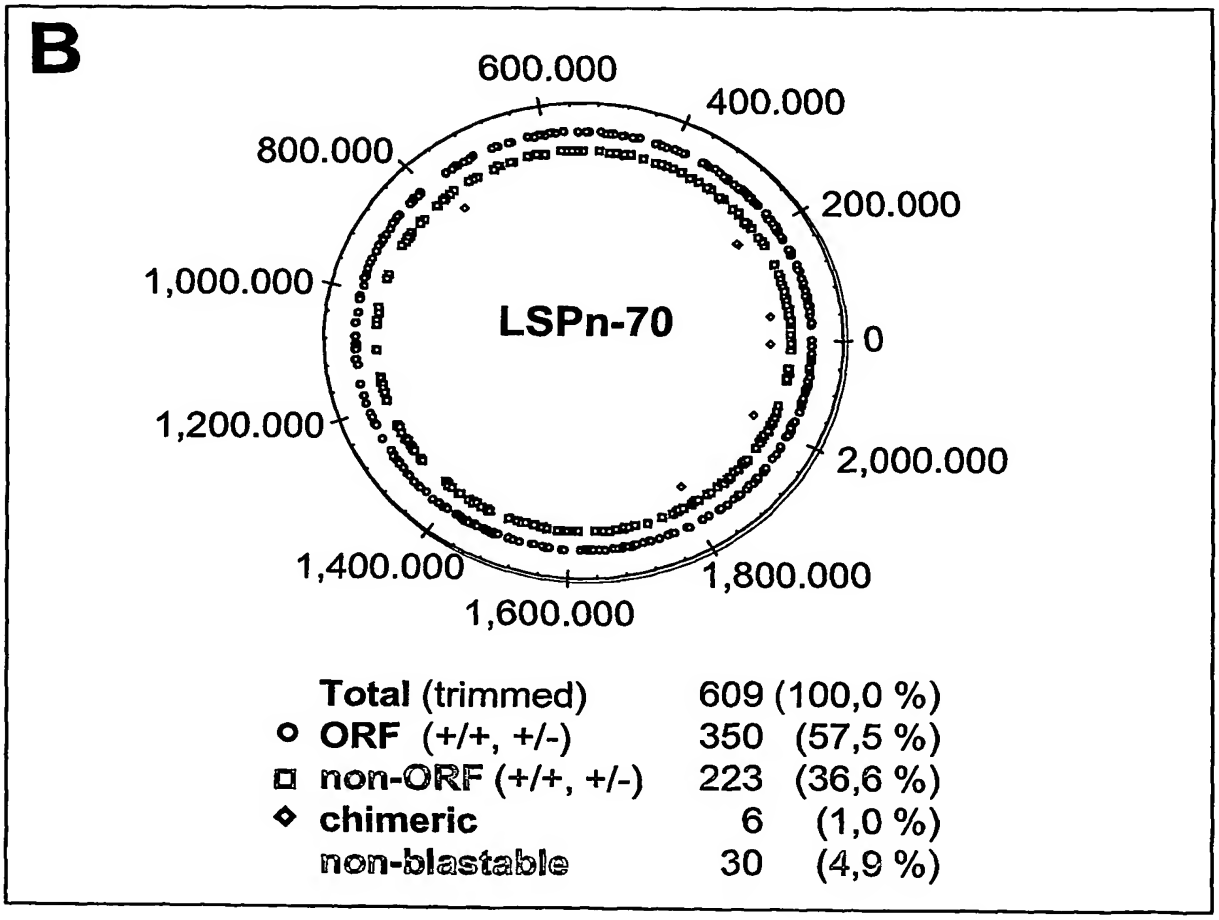

B
600.000
400.000
800.000
200.000
1,000.000
LSPn-70
0
1,200.000
2,000.000
1,400.000
1,800.000
1,600.000
Total (trimmed) 609 (100,0 %)
ORF (+/+, +/-) 350 (57,5 %)
non-ORF (+/+, +/-) 223 (36,6 %)
chimeric 6 (1,0 %)
non-blastable 30 (4,9 %)

Fig. 2

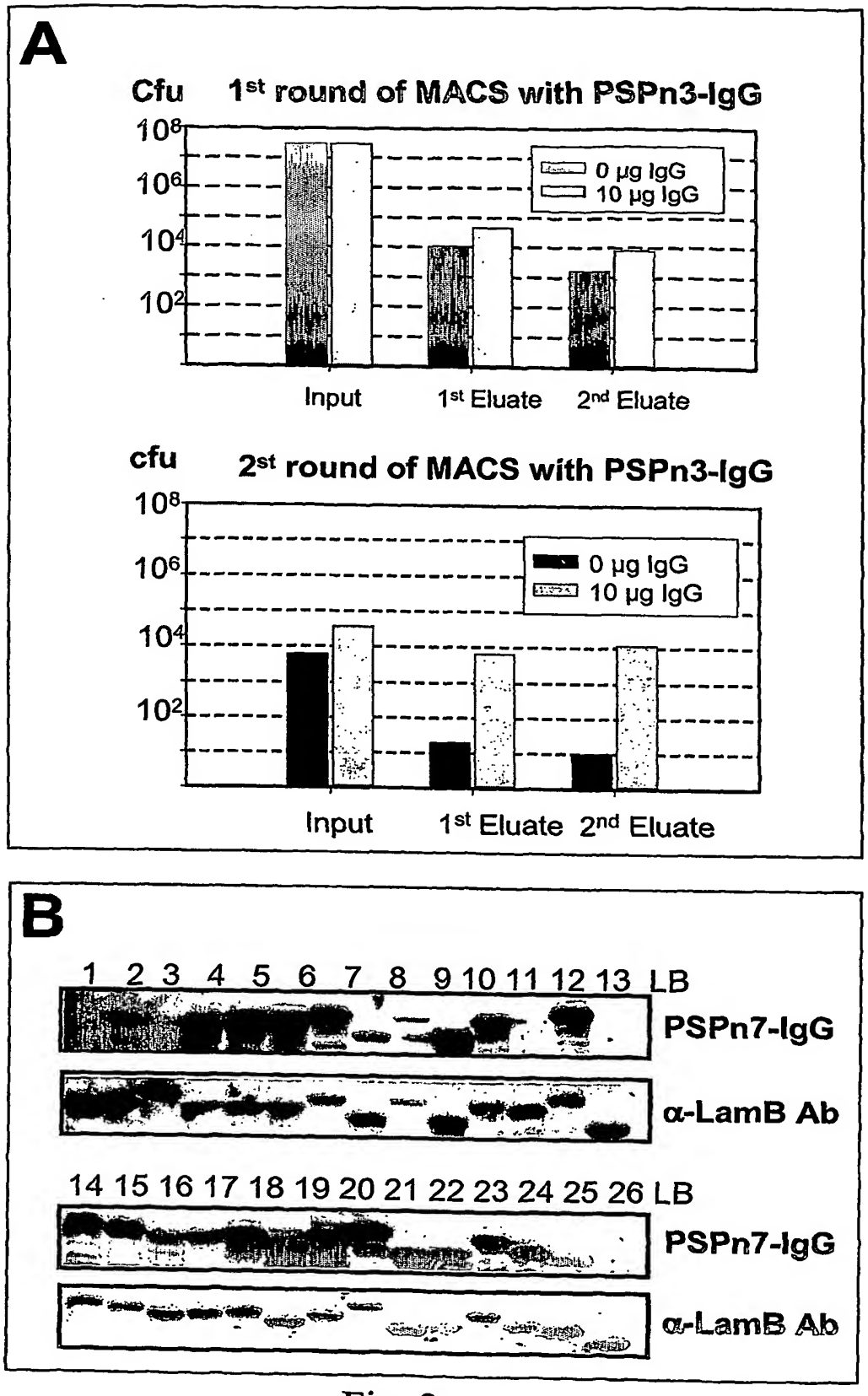
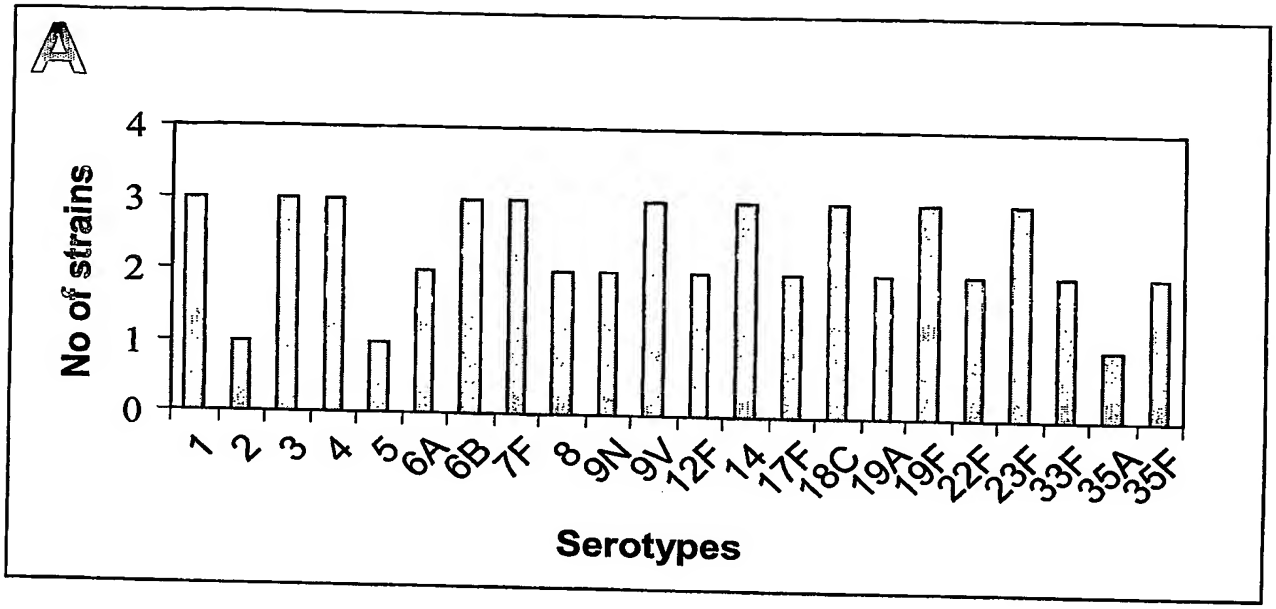

A
Cfu 1st round of MACS with PSPn3-IgG
10^8
10^6
10^4
10^2
0 µg IgG
10 µg IgG
Input
1st Eluate
2nd Eluate
cfu 2st round of MACS with PSPn3-IgG
10^8
10^6
10^4
10^2
0 µg IgG
10 µg IgG
Input
1st Eluate
2nd Eluate
B
1 2 3 4 5 6 7 8 9 10 11 12 13 LB
PSPn7-IgG
α-LamB Ab
14 15 16 17 18 19 20 21 22 23 24 25 26 LB
PSPn7-IgG
α-LamB Ab

Fig. 3


A
No of strains
0
1
2
3
4
1 2 3 4 5 6A 6B 7F 8 9N 9V 12F 14 17F 18C 19A 19F 22F 23F 33F 35A 35F
Serotypes

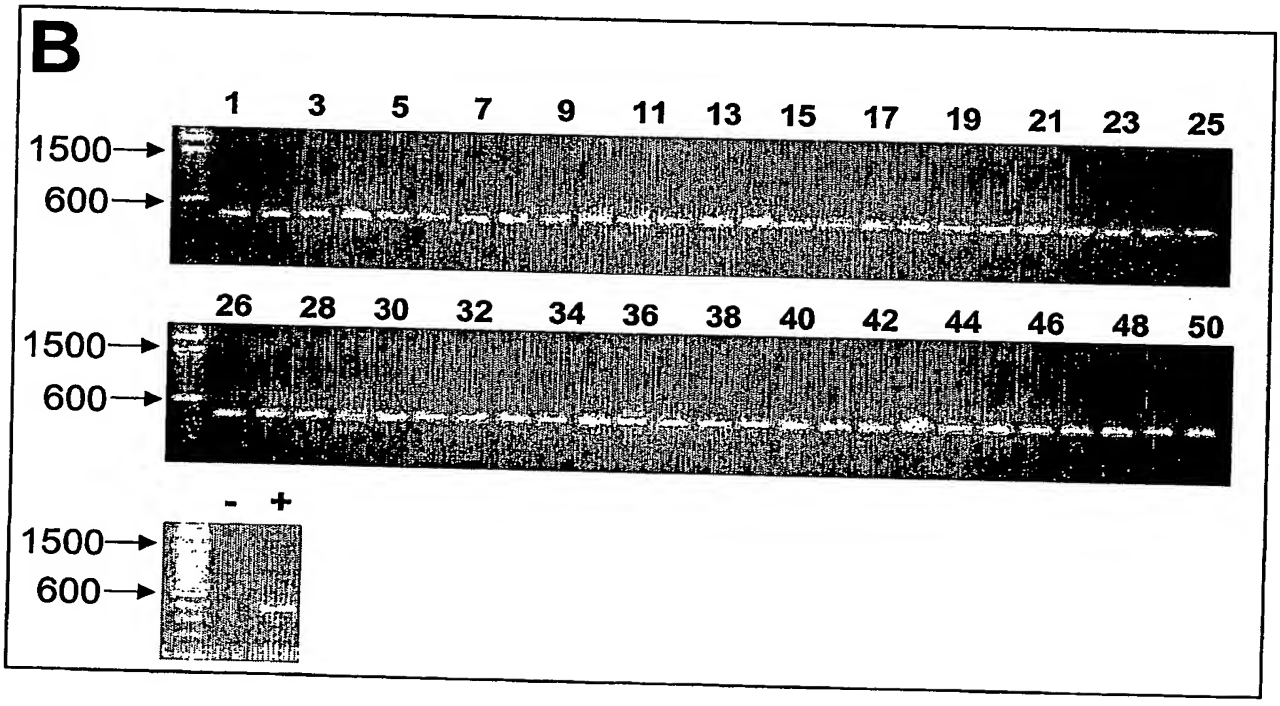

B
1 3 5 7 9 11 13 15 17 19 21 23 25
1500
600
26 28 30 32 34 36 38 40 42 44 46 48 50
1500
600
- +
1500
600

Fig. 4

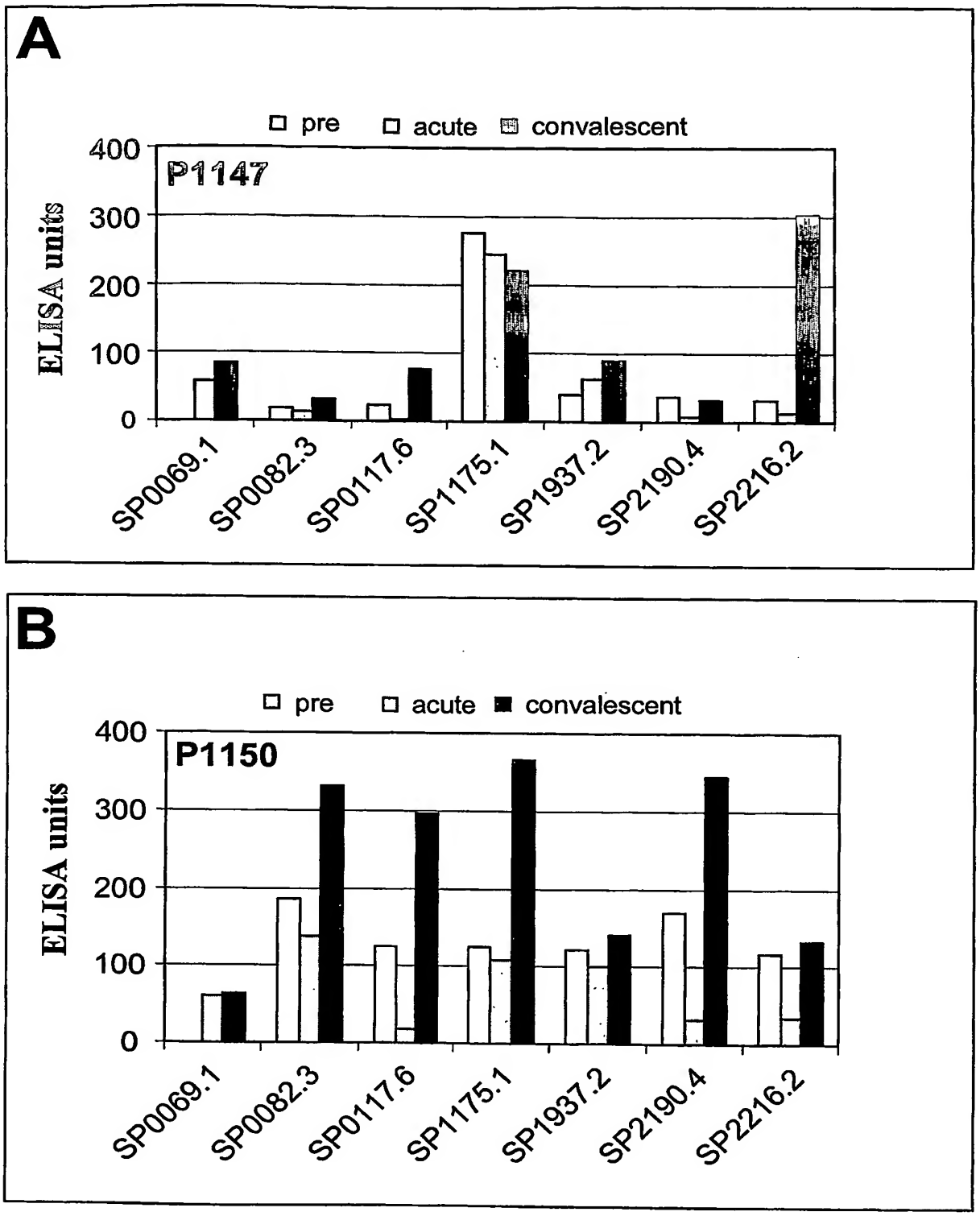

A
pre
acute
convalescent
P1147
ELISA units
400
300
200
100
0
SP0069.1
SP0082.3
SP0117.6
SP1175.1
SP1937.2
SP2190.4
SP2216.2
B
pre
acute
convalescent
P1150
ELISA units
400
300
200
100
0
SP0069.1
SP0082.3
SP0117.6
SP1175.1
SP1937.2
SP2190.4
SP2216.2

Fig. 5

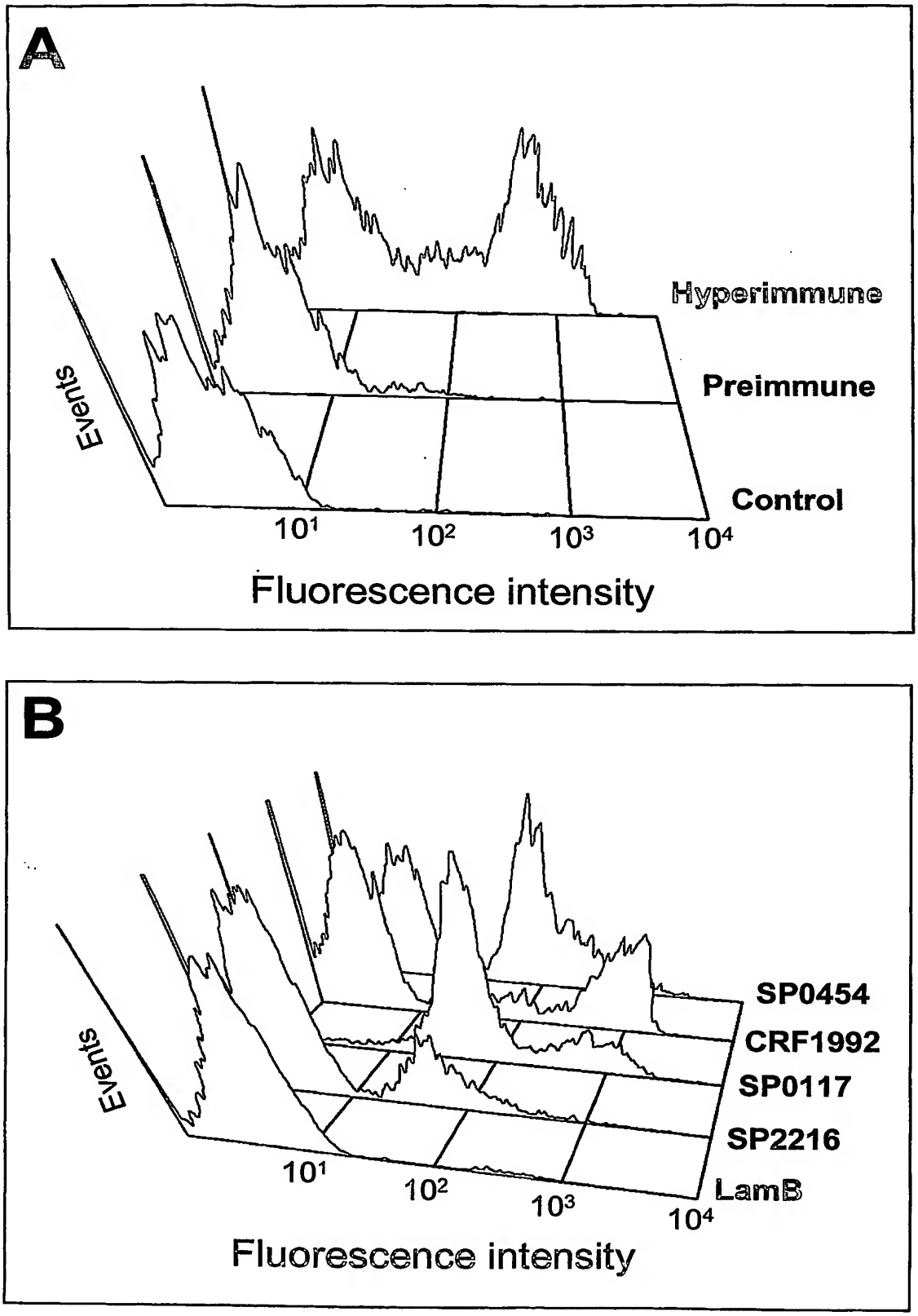

A
Hyperimmune
Preimmune
Control
Events
10¹
10²
10³
10⁴
Fluorescence intensity
B
SP0454
CRF1992
SP0117
SP2216
LamB
Events
10¹
10²
10³
10⁴
Fluorescence intensity

Fig. 6

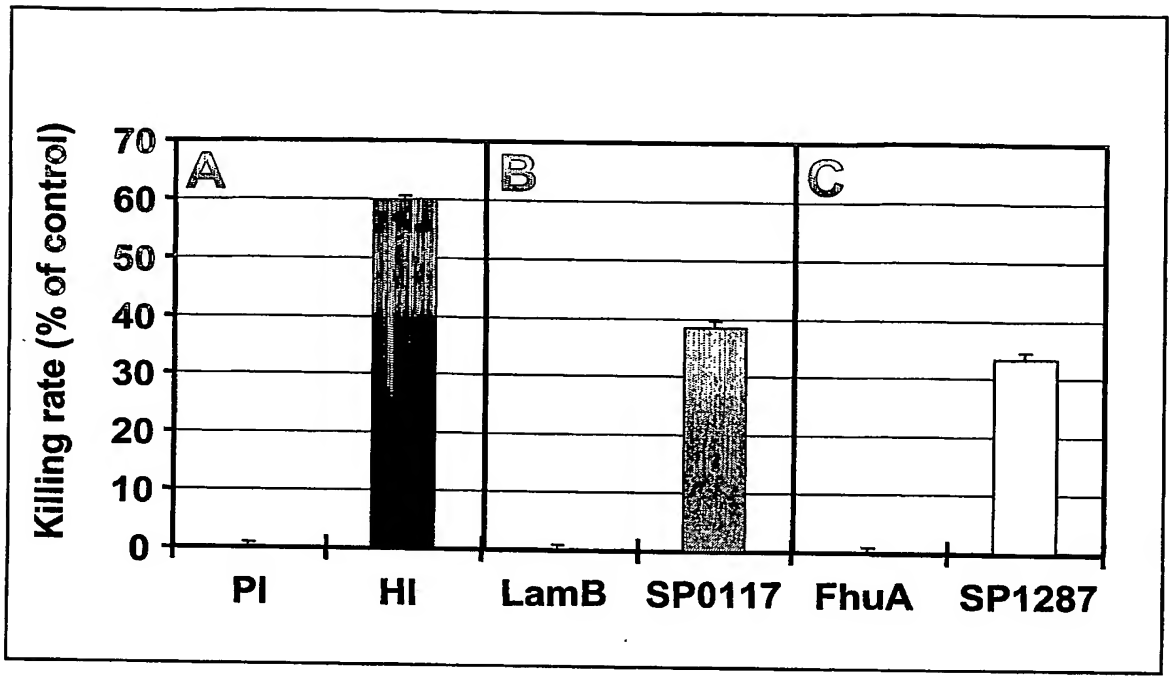
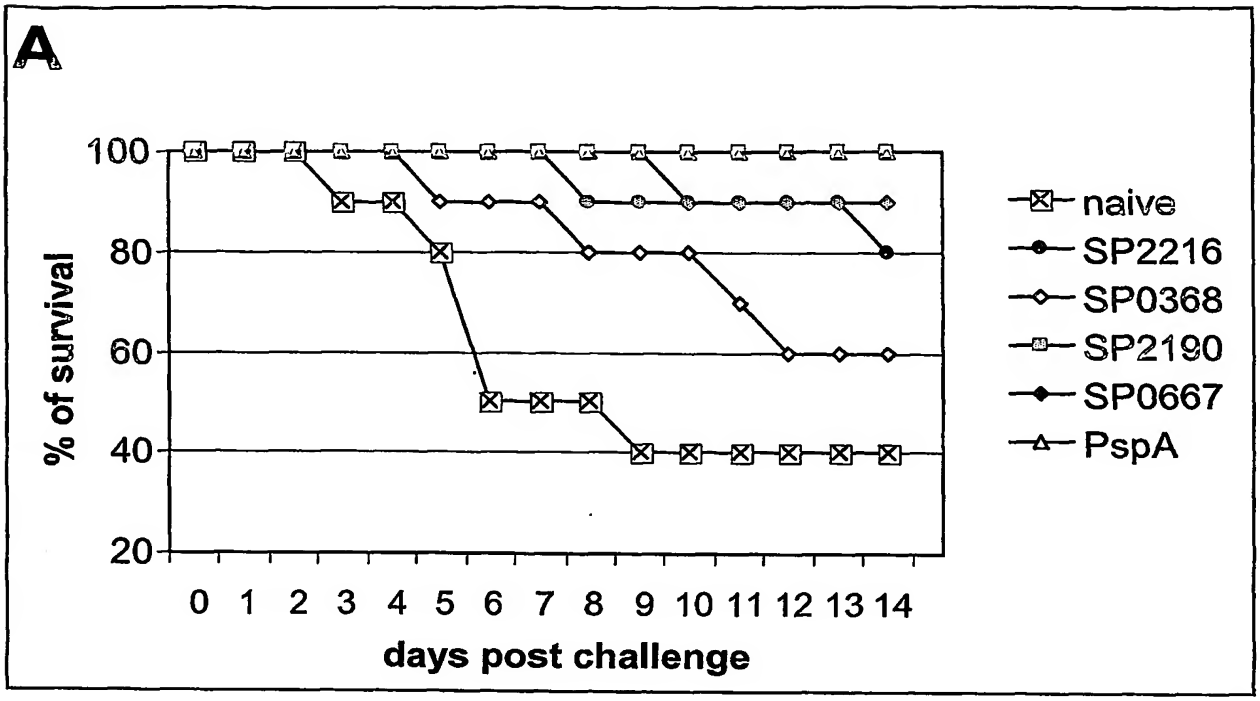

Killing rate (% of control)
70
60
50
40
30
20
10
0
A
B
C
PI
HI
LamB
SP0117
FhuA
SP1287

Fig. 7


A
100
80
60
40
20
% of survival
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
days post challenge
naive
SP2216
SP0368
SP2190
SP0667
PspA

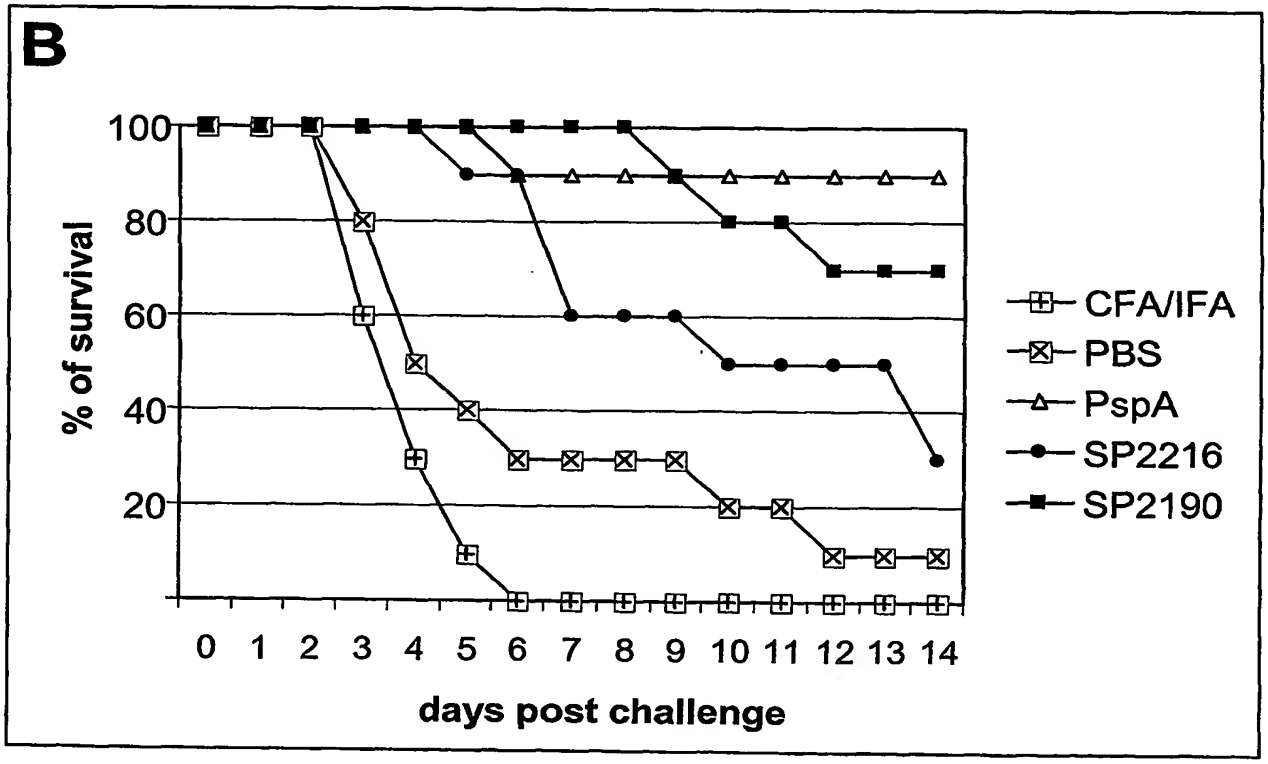

B
100
80
60
40
20
% of survival
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
days post challenge
CFA/IFA
PBS
PspA
SP2216
SP2190

Fig. 8

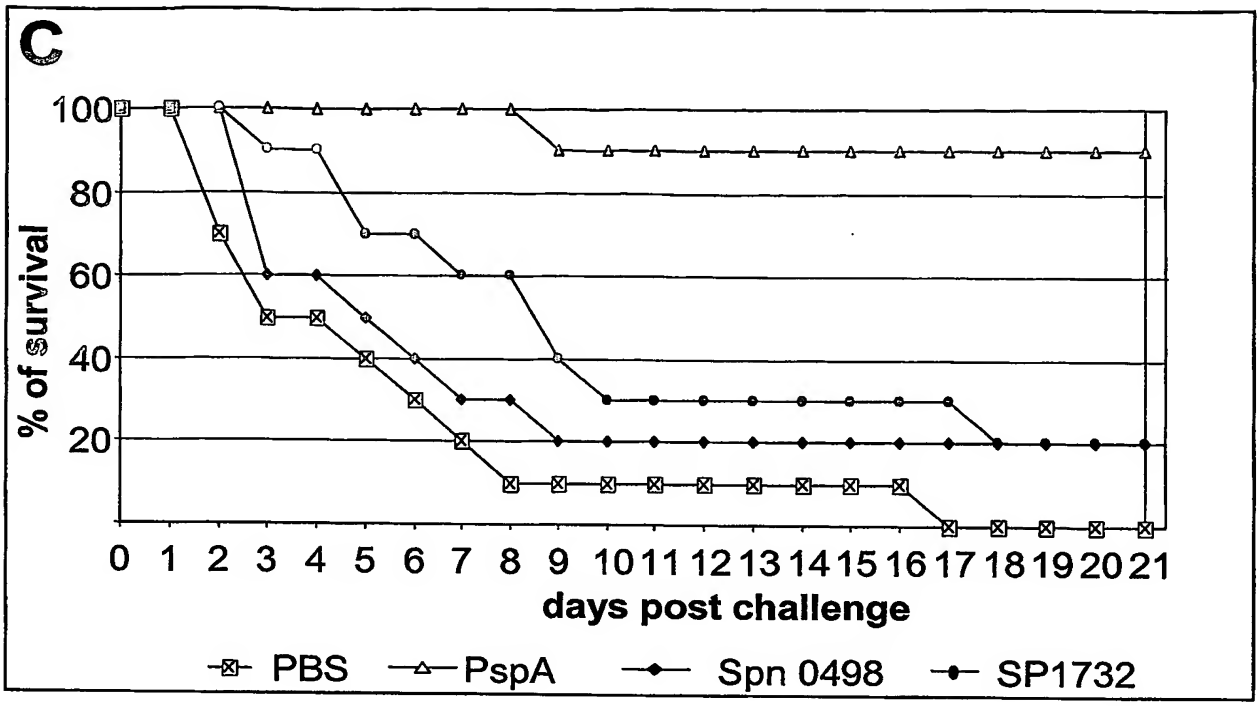

C
100
80
60
40
20
% of survival
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
days post challenge
PBS
PspA
Spn 0498
SP1732

Fig. 8

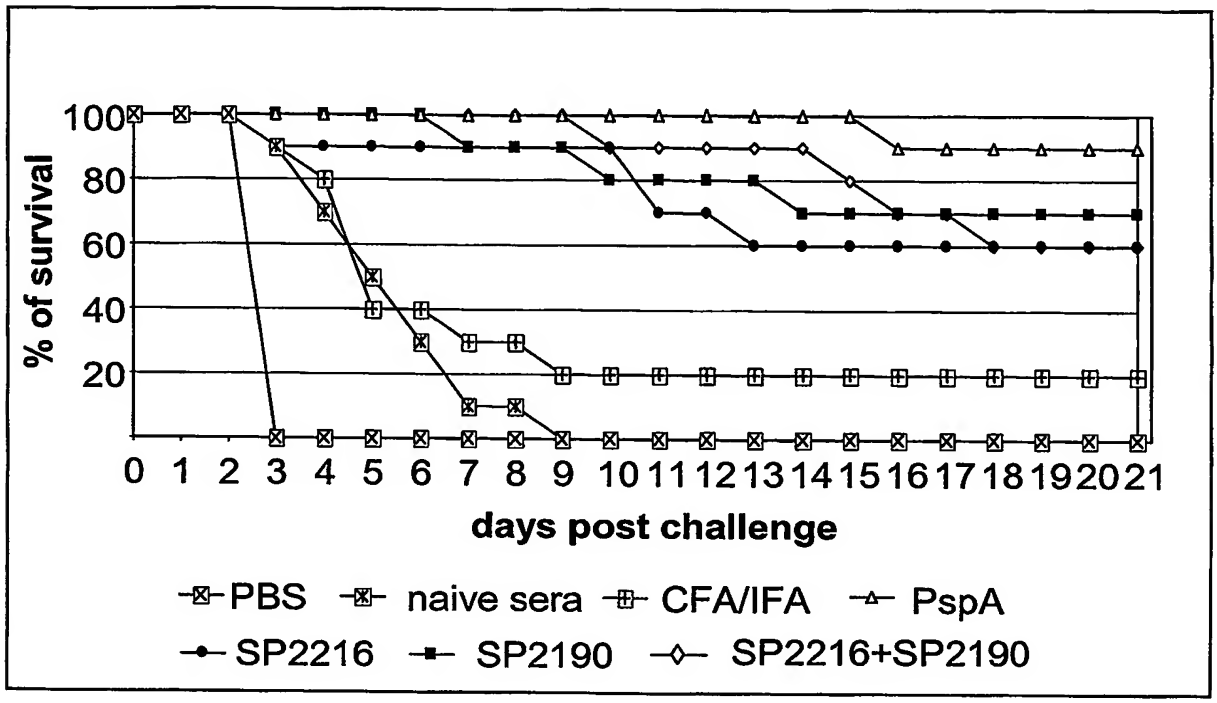
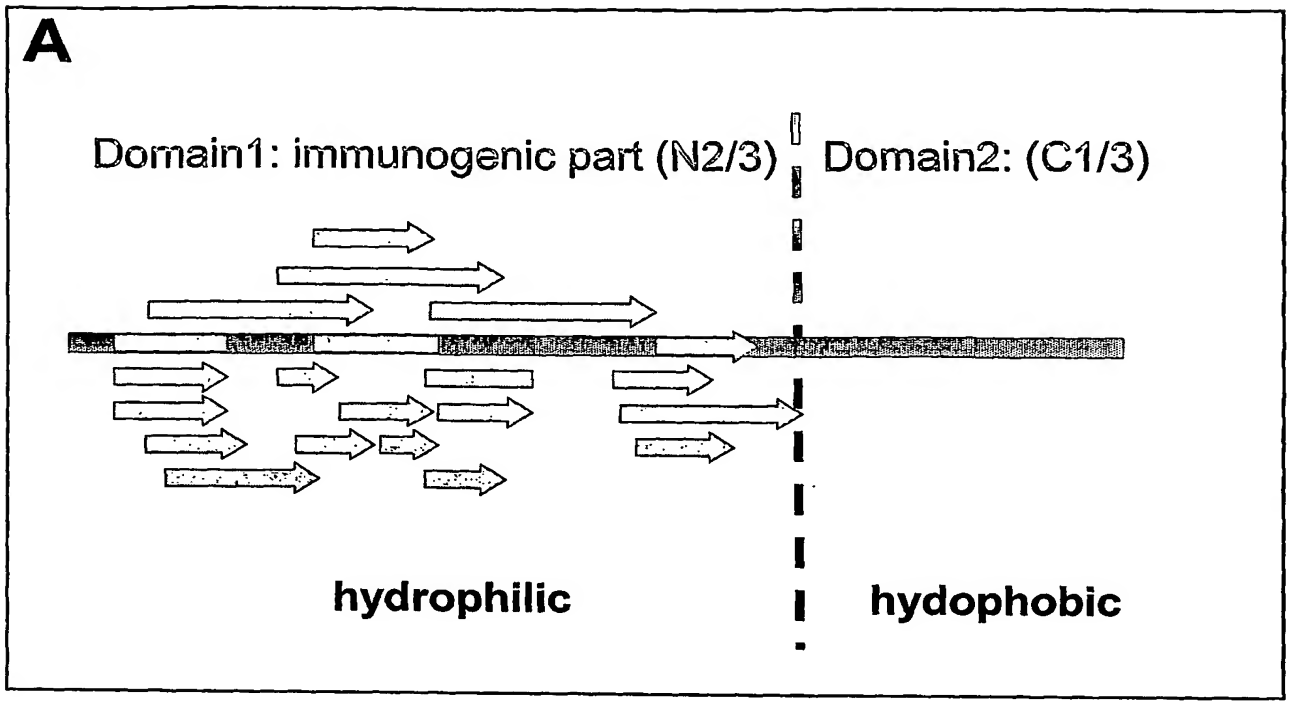

% of survival
100
80
60
40
20
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
days post challenge
PBS
naive sera
CFA/IFA
PspA
SP2216
SP2190
SP2216+SP2190

Fig. 9


A
Domain1: immunogenic part (N2/3)
Domain2: (C1/3)
hydrophilic
hydophobic

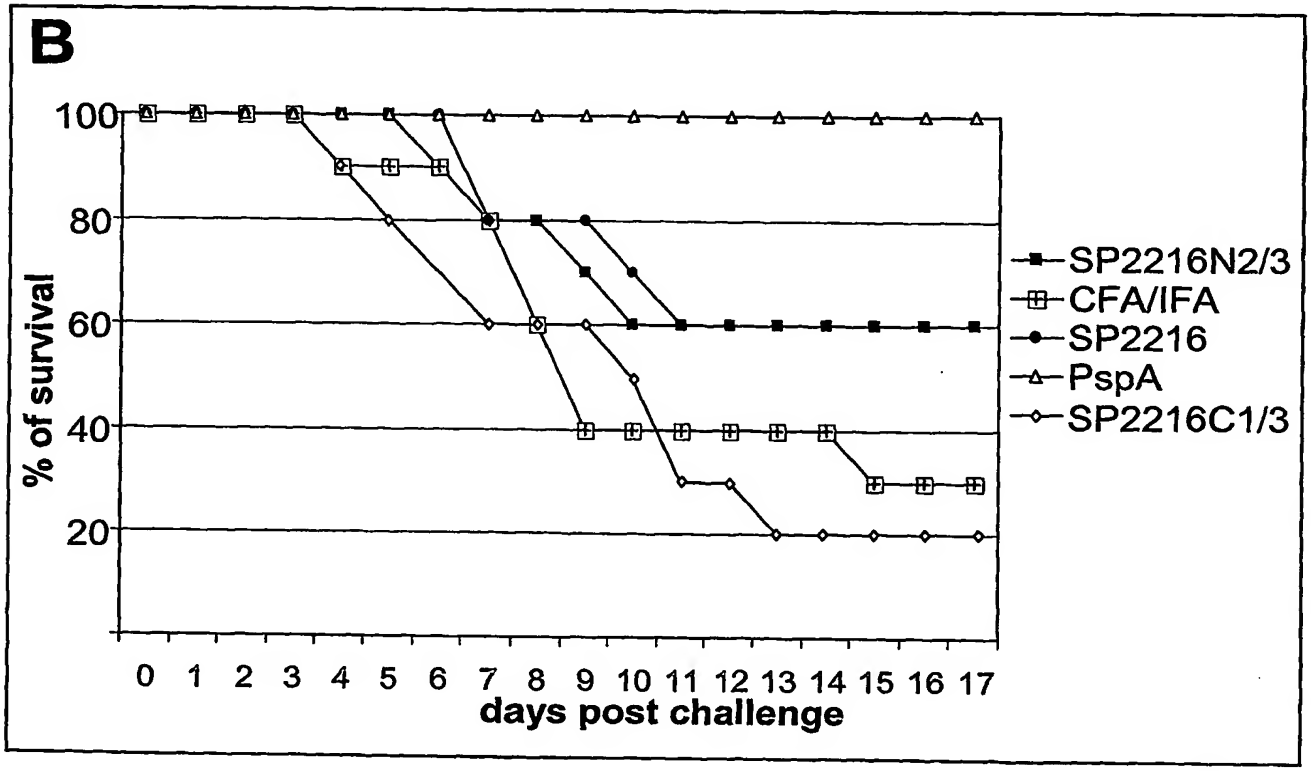

B
100
80
60
40
20
% of survival
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
days post challenge
SP2216N2/3
CFA/IFA
SP2216
PspA
SP2216C1/3

Fig. 10

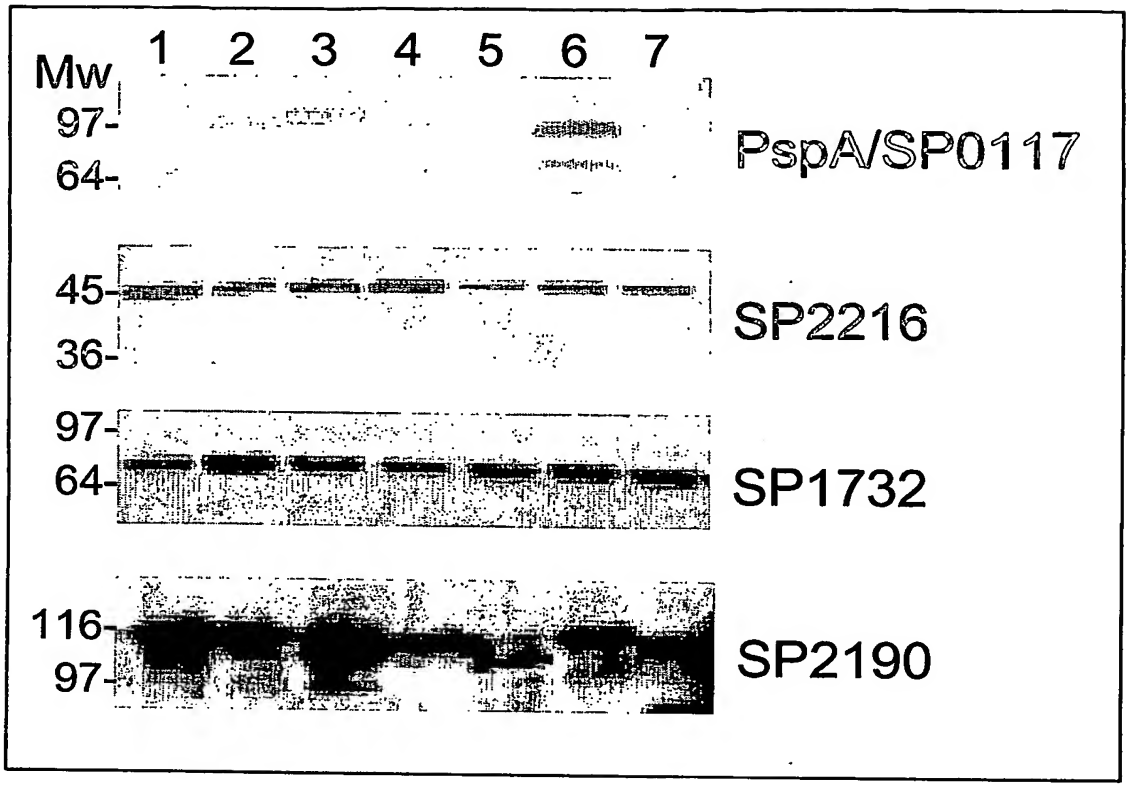

Mw
1 2 3 4 5 6 7
97-
64-
PspA/SP0117
45-
36-
SP2216
97-
64-
SP1732
116-
97-
SP2190

Fig. 11

```
           1                                                                                                        90
TIGR4      MKKKILASLL LSTVMVSQVA VLTTAHAETT DDKIAAQDNK ISNLTAQQQE AQKQVDQIQE QVSAIQAEQS NLQAENDRLQ AESKKLEGEI
14         MKKKILASLL LSTVMVSQVA VLTTAHAETT DDKIAAQDNK ISNLTAQQQE AQKQVDQIQE QVSAIQAEQS NLQAENDRLQ AESKKLEGEI
19F        MKKKILASLL LSTVMVSQVA VLTTAHAETT DDKIAAQDNK ISNLTAQQQE AQKQVDQIQE QVSAIQAEQS NLQAENDRLQ AESKKLEGEI
Consensus  mKKKILASLL LSTVMVSQVA VLTTAHAETT DDKIAAQDNK ISNLTAQQQE AQKQVDQIQE QVSAIQAEQS NLQAENDRLQ AESKKLEGEI

           91                                                                                                      180
TIGR4      TELSKNIVSR NQSLEKQARS AQTNGAVTSY INTIVNSKSI TEAISRVAAM SEIVSANNKM LEQQKADKKA ISEKQVANND AINTVIANQQ
14         TELSKNIVSR NQSLEKQARS AQTNGAVTSY INTIVNSKSI TEAISRVAAM SEIVSANNKM LEQQKADKKA ISEKQVANND AINTVIANQQ
19F        TELSKNIVSR NQSLEKQARS AQTNGAVTSY INTIVNSKSI TEAISRVAAM SEIVSANNKM LEQQKADKKA ISEKQVANND AINTVIANQQ
Consensus  TELSKNIVSR NQSLEKQARS AQTNGAVTSY INTIVNSKSI TEAISRVAAM SEIVSANNKM LEQQKADKKA ISEKQVANND AINTVIANQQ

           181                                                                                                     270
TIGR4      KLADDAQALT TKQAELKAAE LSLAAEKATA EGEKASLLEQ KAAAEAEARA AAVAEAAYKE KRASQQQSVL ASANTNLTAQ VQAVSESAAA
14         KLADDAQALT TKQAELKAAE LSLAAEKATA EGEKASLLEQ KAAAEAEARA AAVAEAAYKE KRASQQQSVL ASANTNLTAQ VQAVSESAAA
19F        KLADDAQALT TKQAELKAAE LSLAAEKATA EGEKASLLEQ KAAAEAEARA AAVAEAAYKE KRAGQQQSVL ASANTNLTAQ VQAVSESAAA
Consensus  KLADDAQALT TKQAELKAAE LSLAAEKATA EGEKASLLEQ KAAAEAEARA AAVAEAAYKE KRAsQQQSVL ASANTNLTAQ VQAVSESAAA

           271                                                                                                     360
TIGR4      PVRAKVRPTY STNASSYPIG ECTWGVKTLA PWAGDYWGNG AQWATSAAAA GFRTGSTPQV GAIACWNDGG YGHVAVVTAV ESTTRIQVSE
14         PVRAKVRPTY STNASSYPIG ECTWGVKTLA PWAGDYWGNG AQWATSAAAA GFRTGSTPQV GAIACWNDGG YGHVAVVTAV ESTTRIQVSE
19F        PVRAKVRPTY STNASSYPIG ECTWGVKTLA PWAGDYWGNG AQWATSAAAA GFRTGSTPQV GAIACWNDGG YGHVAVVTAV ESTTRIQVSE
Consensus  PVRAKVRPTY STNASSYPIG ECTWGVKTLA PWAGDYWGNG AQWATSAAAA GFRTGSTPQV GAIACWNDGG YGHVAVVTAV ESTTRIQVSE

           361                          392
TIGR4      SNYAGNRTIG NHRGWFNPTT TSEGFVTYIY AD
14         SNYAGNRTIG NHRGWFNPTT TPEGFVTYIY AD
19F        SNYAGNRTIG NHRGWFNPTT TSEGFVTYIY AD
Consensus  SNYAGNRTIG NHRGWFNPTT TsEGFVTyiy ad
```

Fig. 12

```
       1                                                                                                 90
TIGR4  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM
    4  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM
   6B  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM
   9V  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM
  18C  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM
   R6  MIQIGKIFAG RYRIVKQIGR GGMADVYLAK DLILDGEEVA VKVLRTNYQT DPIAVARFQR EARAMADLDH PHIVRITDIG EEDGQQYLAM

       91                                                                                               180
TIGR4  EYVAGLDLKR YIKEHYPLSN EEAVRIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS
    4  EYVAGLDLKR YIKEHYPLSN EEAARIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS
   6B  EYVAGLDLKR YIKEHYPLSN EEAVRIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS
   9V  EYVAGLDLKR YIKEHYPLSN EEAVRIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS
  18C  EYVAGLDLKR YIKEHYPLSN EEAVRIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS
   R6  EYVAGLDLKR YIKEHYPLSN EEAVRIMGQI LLAMRLAHTR GIVHRDLKPQ NILLTPDGTA KVTDFGIAVA FAETSLTQTN SMLGSVHYLS

       181                                                                                              270
TIGR4  PEQARGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQKPLP SVIAENPSVP QALENVIIKA TAKKLTNRYR SVSEMYVDLS
    4  PEQAGGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQKPLP SVIAENPSVP QALENVIIKA TAKKLTNRYR SVSEMYVDLS
   6B  PEQARGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQKPLP SVIAENPSVP QALENVIIKA TAKKLTNRYR SVSEMYVDLS
   9V  PEQARGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQKPLP SVIAENPSVP QALENVIIKA TAKKLTNRYR SVSEMYVDLS
  18C  PEQARGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQKPLP SVIAENPSVP QALENVIIRA TAKKLTNRYR SVSEMYVDLS
   R6  PEQARGSKAT VQSDIYAMGI IFYEMLTGHI PYDGDSAVTI ALQHFQNPLP SVIAENSSVP QALENVIIKA TAKKLTNRYR SVSEMYVDLS

       271                                                                                              360
TIGR4  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTEHKSIK NPSQAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
    4  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTEHKSIK NPSQAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
   6B  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTEHKSIK NPSQAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
   9V  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTEHKSIK NPSRAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
  18C  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTGHKSIK NPSQAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
   R6  SSLSYNRRNE SKLIFDETSK ADTKTLPKVS QSTLTSIPKV QAQTEHKSIK NPSQAVTEET YQPQAPKKHR FKMRYLILLA SLVLVAASLI
```

Fig. 13

```
       361                                                                                                   450
TIGR4  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD
    4  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD
   6B  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD
   9V  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD
  18C  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD
   R6  WILSRTPATI AIPDVAGQTV AEAKATLKKA NFEIGEEKTE ASEKVEEGRI IRTDPGAGTG RKEGTKINLV VSSGKQSFQI SNYVGRKSSD

       451                                                                                                   540
TIGR4  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQIV LTVAKKATTI QLGNYIGRNS TEVISELKQK KVPENLIKIE
    4  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQI- ---------- ---------- ---------- ----------
   6B  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQIV LTVAKKATTI QLGNYIGRNS TEVISELKQK KVPENLIKIE
   9V  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQIV LTVAKKATTI QLGNYIGRNS TEVISELKQK KVPENLIKIE
  18C  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQII LTVAKKATTI QLGNYIGRNS TEVISELKQK KVPENLIKIE
   R6  VIAELKEKKV PDNLIKIEEE ESNESEAGTV LKQSLPEGTT YDLSKATQIV LTVAKKATTI QLGNYIGRNS TEVISELKQK KVPENLIKIE

       541                                                                                                   630
TIGR4  EEESSESEPG TIMKQSPGAG TTYDVSKPTQ IVLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSAEGMVVEQ
    4  ---------- ---------- ---------- -VLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSAEGMVVEQ
   6B  EEESSESEPG TIMKQSPGAG TTYDVSKPTQ IVLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSVEGMVVEQ
   9V  EEESSESEPG TIMKQSPGAG TTYDVSKPTQ IVLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSAEGMVVEQ
  18C  EEESSESEPG TIMKQSPGAG TTYDVSKPTQ IVLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSAEGMVVEQ
   R6  EEESSESEPG TIMKQSPGAG TTYDVSKPTQ IVLTVAKKVT SVAMPSYIGS SLEFTKNNLI QIVGIKEANI EVVEVTTAPA GSVEGMVVEQ

       631                  659
TIGR4  SPRAGEKVDL NKTRVKISIY KPKTTSATP
    4  SPRAGEKVDL NKTRVKISIY KPKTTSATP
   6B  SPRAGEKVDL NKTRVKISIY KPKTTSATP
   9V  SPRAGEKVDL NKTRVKTSIY KPKTTSATP
  18C  SPRAGEKVDL NKTRVKISIY KPKTTSATP
   R6  SPRAGEKVDL NKTRVKISIY KPKTTSATP
```

Fig. 13

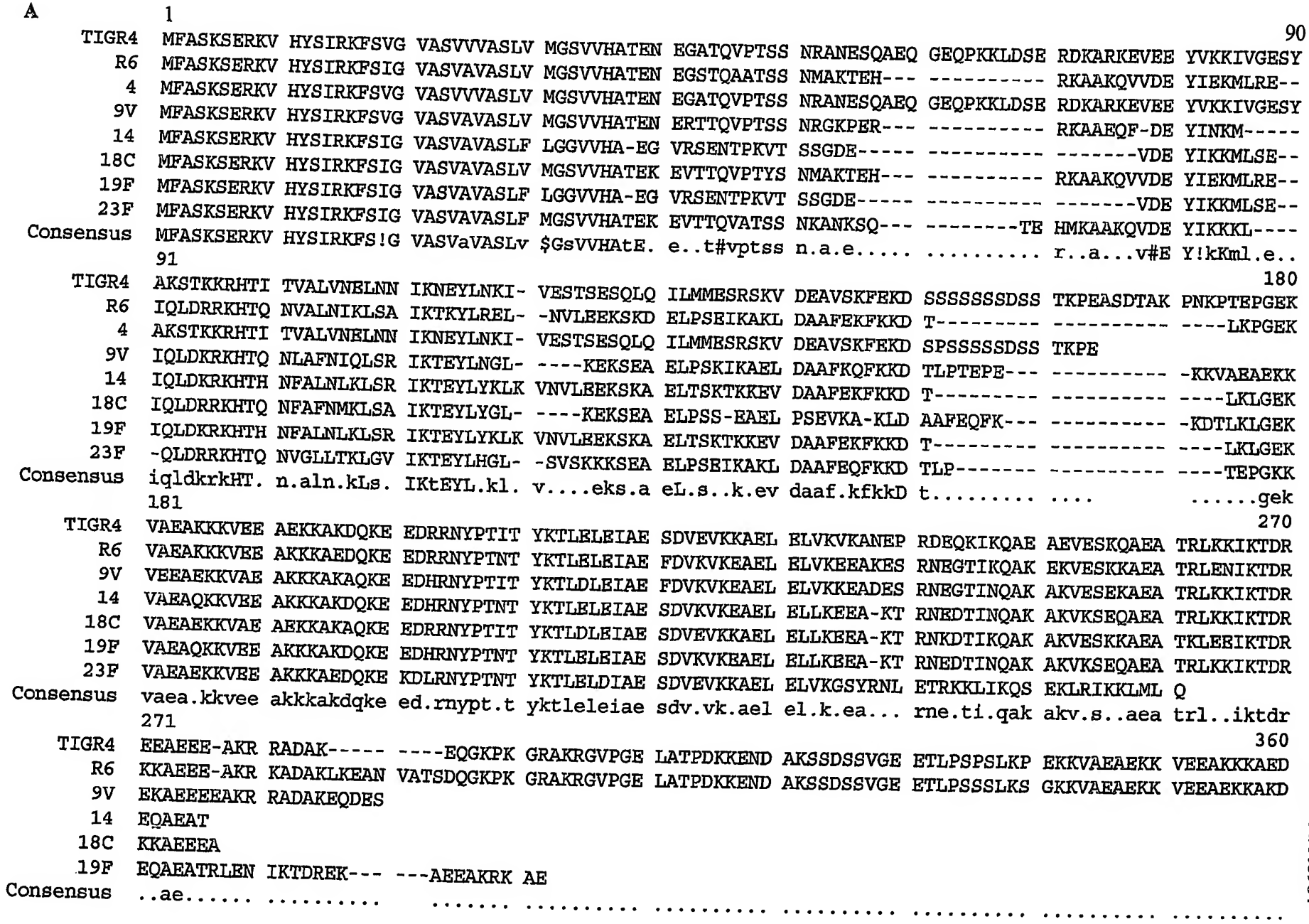

A
1
90
TIGR4 MFASKSERKV HYSIRKFSVG VASVVVASLV MGSVVHATEN EGATQVPTSS NRANESQAEQ GEQPKKLDSE RDKARKEVEE YVKKIVGESY
R6 MFASKSERKV HYSIRKFSIG VASVAVASLV MGSVVHATEN EGSTQAATSS NMAKTEH--- ---------- RKAAKQVVDE YIEKMLRE--
4 MFASKSERKV HYSIRKFSVG VASVVVASLV MGSVVHATEN EGATQVPTSS NRANESQAEQ GEQPKKLDSE RDKARKEVEE YVKKIVGESY
9V MFASKSERKV HYSIRKFSVG VASVAVASLV MGSVVHATEN ERTTQVPTSS NRGKPER--- ---------- RKAAEQF-DE YINKM-----
14 MFASKSERKV HYSIRKFSIG VASVAVASLF LGGVVHA-EG VRSENTPKVT SSGDE----- ---------- -------VDE YIKKMLSE--
18C MFASKSERKV HYSIRKFSIG VASVAVASLV MGSVVHATEK EVTTQVPTYS NMAKTEH--- ---------- RKAAKQVVDE YIEKMLRE--
19F MFASKSERKV HYSIRKFSIG VASVAVASLF LGGVVHA-EG VRSENTPKVT SSGDE----- ---------- -------VDE YIKKMLSE--
23F MFASKSERKV HYSIRKFSIG VASVAVASLF MGSVVHATEK EVTTQVATSS NKANKSQ--- --------TE HMKAAKQVDE YIKKKL----
Consensus MFASKSERKV HYSIRKFS!G VASVaVASLv $GsVVHAtE. e..t#vptss n.a.e..... .... r..a...v#E Y!kKml.e..
91
TIGR4 AKSTKKRHTI TVALVNELNN IKNEYLNKI- VESTSESQLQ ILMMESRSKV DEAVSKFEKD SSSSSSSDSS TKPEASDTAK PNKPTEPGEK
R6 IQLDRRKHTQ NVALNIKLSA IKTKYLREL- -NVLEEKSKD ELPSEIKAKL DAAFEKFKKD T---------- ---------- ----LKPGEK
4 AKSTKKRHTI TVALVNELNN IKNEYLNKI- VESTSESQLQ ILMMESRSKV DEAVSKFEKD SPSSSSSDSS TKPE
9V IQLDKRKHTQ NLAFNIQLSR IKTEYLNGL- ----KEKSEA ELPSKIKAEL DAAFKQFKKD TLPTEPE--- ---------- -KKVAEAEKK
14 IQLDKRKHTH NFALNLKLSR IKTEYLYKLK VNVLEEKSKA ELTSKTKKEV DAAFEKFKKD T---------- ---------- ----LKLGEK
18C IQLDRRKHTQ NFAFNMKLSA IKTEYLYGL- ----KEKSEA ELPSS-EAEL PSEVKA-KLD AAFEQFK--- ---------- -KDTLKLGEK
19F IQLDKRKHTH NFALNLKLSR IKTEYLYKLK VNVLEEKSKA ELTSKTKKEV DAAFEKFKKD T---------- ---------- ----LKLGEK
23F -QLDRRKHTQ NVGLLTKLGV IKTEYLHGL- -SVSKKKSEA ELPSEIKAKL DAAFEQFKKD TLP------- ---------- ----TEPGKK
Consensus iqldkrkHT. n.aln.kLs. IKtEYL.kl. v....eks.a eL.s..k.ev daaf.kfkkD t..... ....gek
181
TIGR4 VAEAKKKVEE AEKKAKDQKE EDRRNYPTIT YKTLELEIAE SDVEVKKAEL ELVKVKANEP RDEQKIKQAE AEVESKQAEA TRLKKIKTDR
R6 VAEAKKKVEE AKKKAEDQKE EDRRNYPTNT YKTLELEIAE FDVKVKEAEL ELVKEEAKES RNEGTIKQAK EKVESKKAEA TRLENIKTDR
9V VEEAEKKVAE AKKKAKAQKE EDHRNYPTIT YKTLDLEIAE FDVKVKEAEL ELVKKEADES RNEGTINQAK AKVESEKAEA TRLKKIKTDR
14 VAEAQKKVEE AKKKAKDQKE EDHRNYPTNT YKTLELEIAE SDVKVKEAEL ELLKEEA-KT RNEDTINQAK AKVKSEQAEA TRLKKIKTDR
18C VAEAEKKVAE AEKKAKAQKE EDRRNYPTIT YKTLDLEIAE SDVEVKKAEL ELLKEEA-KT RNKDTIKQAK AKVESKKAEA TKLEEIKTDR
19F VAEAQKKVEE AKKKAKDQKE EDHRNYPTNT YKTLELEIAE SDVKVKEAEL ELLKEEA-KT RNEDTINQAK AKVKSEQAEA TRLKKIKTDR
23F VAEAEKKVEE AKKKAEDQKE KDLRNYPTNT YKTLELDIAE SDVEVKKAEL ELVKGSYRNL ETRKKLIKQS EKLRIKKLML Q
Consensus vaea.kkvee akkkakdqke ed.rnypt.t yktleleiae sdv.vk.ael el.k.ea... rne.ti.qak akv.s..aea trl..iktdr
271
TIGR4 EEAEEE-AKR RADAK----- ----EQGKPK GRAKRGVPGE LATPDKKEND AKSSDSSVGE ETLPSPSLKP EKKVAEAEKK VEEAKKKAED
R6 KKAEEE-AKR KADAKLKEAN VATSDQGKPK GRAKRGVPGE LATPDKKEND AKSSDSSVGE ETLPSSSLKS GKKVAEAEKK VEEAEKKAKD
9V EKAEEEEAKR RADAKEQDES
14 EQAEAT
18C KKAEEEA
19F EQAEATRLEN IKTDREK--- ---AEEAKRK AE
Consensus ..ae..... .....

Fig. 14

B

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          361                                                                                                          450
TIGR4     QKEEDRRNYP TNTYKTLELE IAESDVEVKK AELELVKEEA KEPRNEEKVK QAKAEVESKK AEATRLEKIK TDRKKAEEEA KRKAAEEDKV
R6        QKEEDRRNYP TNTYKTLDLE IAESDVKVKE AELELVKEEA KEPRDEEKIK QAKAKVESKK AEATRLENIK TDRKKAEEEA KRKAAEEDKV
4                               AESDVEVKK AELELVKEEA KEPRNEEKVK QAKAEVESKK AEATRLEKIK TDRKKAEEEA KRKAAEEDKV
6B                           LK LLSPMWKLKK RSLTS-KEEA KKPLNEGTIR QAKAEVESKK AEATRLEKIK TDRKKAEEEA KRRAAEEDKV
9V                              IAESDVKVKE AELELVKEEA KESRNEEKIK QAKAKVESKK AEATRLEKIK TDRKKAEEEA KRKAAEEDKV
14                              IAESDVKVKE AELELVKEEA KEPRDEEKIK QAKAEVESKQ AEATRLEKIK TDRKKAEEEA KRKAAEEDKV
18C                             IAESDVKVKE AELELVKEEA KESRNEEKVK QAKAKVESKK AEATRLEKIK TDRKKAEE-A KRRAAEEDKV
19F                          LE IAESDVKVKE AELELVKEEA KESRNEEKVK QAKAKVESKQ AEATRLEKIK TDRKKAEEEA KRKAAEEDKV
23F
Consensus .......... .......... iaesdvkvke aelelvkeea keprneek.k qaka.veskk aeatrlekik tdrkkaeeea krkaaeedkv

          451                                                                                                          540
TIGR4     KEKPAEQPQP APAPKAEKPA -------PAP KPENPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
R6        KEKPAEQPQP APATQPEKPA -------P-- KPEKPAEQPK AEKTD----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
4         KEKPAEQPQP APAPKAEKP- ------APAP KPENPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
6B        KEKPAEQPQP APAPQPEKPT EEPENPVPAP KPEKPAEQPK PEKPAEQPKP EKPAEQPKAE KTDDQQAEED YARRSEEEYN RLTQQQPQKP
9V        KEKPAEQPQP APAPKPENPA EEPENPVPAP KPENPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKP
14        KEKPAEQPQP APAPQPEKPT PKPEKPAPAP KPENPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
18C       KEKPAEQPQP APAPQPEKPT EEPENPAPAP KPEKPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
19F       KEKPAEQPQP APAPQPEKP- ------APAP KPENPAEQPK AEKPA----- ---------- ---DQQAEED YARRSEEEYN RLTQQQPPKT
23F                                                                           VQNGMW YFYNTDGSMA TGWLQNNGSW
Consensus kekpaeqpqp apapqpekp. .......pap kpenpaeqpk aekpa..... .......... ...dqQaeed Yarrs#eeyn rltqQ#ppkt

          541                                                                                                          630
TIGR4     EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQNNGSW YYLNSNGAMA TGWLQNNGSW YYLNANGSMA TGWLQNNGSW YYLNANGSMA
R6        EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQNNGSW YYLNANGAMA TGWLQNNGSW YYLNANGSMA TGWLQNNGSW YYLNANGAMA
4         EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQNNGSW YYLNSNGAMA TGWLQNNGSW YYLNANGSMA TGWLQNNGSW YYLNANGSMA
6B        EQPAP--APK IGWKQENGMW YFYNTDGSMA TGWLQ----- ---------- ---------- ---------- ---------- ----------
9V        EQPAP--APK IGWKQENGMW YFYNTDGSMA TGWLQNNGSW YYLNSNGAMA TGWLQNNGSW YYLNANGSMA TGWLQNNGSW YYLNANGDMA
14        EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQYNGSW YYLNANGDMA TGWLQNNGSW YYLNANGDMA TGWLQNNGSW YYLNANG---
18C       EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQNNGSW YYLNSNGAMA TGWLQYNGSW YYLNANGDMA TGWLQNNGSW YYLNANGDMA
19F       EKPAQPSTPK TGWKQENGMW YFYNTDGSMA TGWLQYNGSW YYLNANGDMA TGWLQNNGSW YYLNANGDMA TGWLQNNGSW YYLNANG---
23F       YYLNSNGAMA TGWLQNNGSW YYLNSNGAMA TGWLQYNGSW YYLNANGDMA TGWFQYNGSW YYLNANGDMA TGWFQYNGSW YYLNANGDMA
Consensus ekpaqpstpk tGWkQ#NGmW Y%yNt#GsMA TGWLQ.ngsw yyln.ng.ma tgwlqnngsw yylnang.ma tgwlqnngsw yylnang.ma
```

Fig. 14

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          631                                                                                                  720
TIGR4     TGWLQYNGSW YYLN------ ---------- ---------- ---------- ----ANGSMA TGWLQYNGSW YYLNANGDMA TGWVKDGDTW
R6        TGWLQYNGSW YYLNSNGAMA TGWLQYNGSW YYLNANGDMA TGWLQNNGSW YYLNANGDMA TGWLQYNGSW YYLNANGDMA TGWVKDGDTW
4         TGWLQYNGSW YYLN------ ---------- ---------- ---------- ----ANGSMA TGWLQYNGSW YYLNANGDMA TGWVKDGDTW
6B        ---------- ---------- ---------- ---------- ---------- ---------- -----YNGSW YYLNANGSMA TGWVKDGDTW
9V        TGWLQYNGSW YYLN------ ---------- ----ANGDMA TGWLQYNGSW YYLNANGDMA TGWLQYNGSW YYLNANGDMA TGWVKDGDTW
14        ---------- ---------- ---------- ---------- ---------- -------DMA TGWLQNNGSW YYLNANGDMA TGWVKDGDTW
18C       TGWLQYNGSW YYLN------ ---------- ---------- ---------- ----ANGDMA TGWLQNNGSW YYLNANGDMA TGWVKDGDTW
19F       ---------- ---------- ---------- ---------- ---------- -------DMA TGWLQNNGSW YYLNANGDMA TGWVKDGDTW
23F       TGWFQYNGSW YYLN------ ---------- ----ANGDMA TGWLQYNGSW YYLNSNGAMV TGWLQNNGSW YYLNANGSMA TDWVKDGDTW
Consensus tgw.qyngsw yyln                  ...... .......... .....ngdma tgwlqyNGSW YYLNANGdMA TgWVKDGDTW

          721                                                769
TIGR4     YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
R6        YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
4         YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
6B        YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
9V        YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
14        YYLEASGAMK ASQWFKASDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
18C       YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
19F       YYLEASGAMK ASQWFKASDK WYYVNGSGAL AVNTTVDGYG VNANGEWVN
23F       YYLEASGAMK ASQWFKVSDK WYYVNGSGAL AVNTTVDSYR VNANGEWVN
Consensus YYLEASGAMk asqwfkvsdk wyyvngsgal avnttvdgyg vnangewvn
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Fig. 14

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